

## **RAW SEQUENCE LISTING**

**The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.**

Application Serial Number: 10/581,223  
Source: IFWP  
Date Processed by STIC: 6/9/06

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IFWP

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/581,223

DATE: 06/09/2006

TIME: 10:38:51

Input Set : A:\Final Sequence list-12810-00260-US.txt  
 Output Set: N:\CRF4\06092006\J581223.raw

3 <110> APPLICANT: Ehrhardt, Thomas  
 4 Reindl, Andreas  
 5 Freund, Annette  
 6 Schmidt, Ralf-Michael  
 7 Sonnewald, Uwe  
 8 Sitt Nigel, Marc  
 9 Lein, Wolfgang  
 10 Bornke, Frederik  
 12 <120> TITLE OF INVENTION: 2-Methyl-6-solanylbenzoquinone methyltransferase as target  
 for  
 13 herbicides  
 15 <130> FILE REFERENCE: 12810-00260-US  
 C--> 17 <140> CURRENT APPLICATION NUMBER: US/10/581,223  
 C--> 17 <141> CURRENT FILING DATE: 2006-06-01  
 17 <150> PRIOR APPLICATION NUMBER: PCT/EP2004/013560  
 18 <151> PRIOR FILING DATE: 2004-11-30  
 20 <150> PRIOR APPLICATION NUMBER: DE 103 56 631.7  
 21 <151> PRIOR FILING DATE: 2003-12-02  
 23 <160> NUMBER OF SEQ ID NOS: 35  
 25 <170> SOFTWARE: PatentIn version 3.3  
 28 <210> SEQ ID NO: 1  
 29 <211> LENGTH: 1355  
 30 <212> TYPE: DNA  
 31 <213> ORGANISM: Nicotiana tabacum  
 33 <220> FEATURE:  
 34 <221> NAME/KEY: CDS  
 35 <222> LOCATION: (110)..(1117)  
 38 <400> SEQUENCE: 1  
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 41 ttatcaaaac tatatgcagt aaaaaaaaaata acatcaaaaa tacatatcc atg gct tct 118  
 42 Met Ala Ser  
 43 1  
 45 tca ata cta agt gga gct gaa aat ttc aag att ctt agt ggt att tct 166  
 46 Ser Ile Leu Ser Gly Ala Glu Asn Phe Lys Ile Leu Ser Gly Ile Ser  
 47 5 10 15  
 49 cca tca gaa tta cac att aag tgt ttt cct caa aag ggt ctt gta aat 214  
 50 Pro Ser Glu Leu His Ile Lys Cys Phe Pro Gln Lys Gly Leu Val Asn  
 51 20 25 30 35  
 53 tac tca aga att cca aat acc aaa tca aga act cta aga aca aaa tgc 262  
 54 Tyr Ser Arg Ile Pro Asn Thr Lys Ser Arg Thr Leu Arg Thr Lys Cys  
 55 40 45 50  
 57 agt gta tca tct tca aga cca gct tca caa cca aga ttt ata caa cac 310  
 58 Ser Val Ser Ser Arg Pro Ala Ser Gln Pro Arg Phe Ile Gln His  
 59 55 60 65

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61	aaa	aaa	gaa	gca	ttt	tgg	ttt	tac	aga	ttc	tta	tct	ata	gta	tat	gac	358
62	Lys	Lys	Glu	Ala	Phe	Trp	Phe	Tyr	Arg	Phe	Leu	Ser	Ile	Val	Tyr	Asp	
63																80	
65	cat	gtt	ata	aat	cca	ggt	cat	tgg	act	gaa	gat	atg	aga	gat	gaa	gca	406
66	His	Val	Ile	Asn	Pro	Gly	His	Trp	Thr	Glu	Asp	Met	Arg	Asp	Glu	Ala	
67																95	
69	ctt	gaa	cca	gct	gaa	tta	aac	agt	aga	caa	ttg	caa	gtt	gtg	gat	gtt	454
70	Leu	Glu	Pro	Ala	Glu	Leu	Asn	Ser	Arg	Gln	Leu	Gln	Val	Val	Asp	Val	
71	100															115	
73	ggt	ggg	act	gga	ttt	act	act	ctt	ggc	att	gtg	aaa	cat	gtg	gat		502
74	Gly	Gly	Gly	Thr	Gly	Phe	Thr	Thr	Leu	Gly	Ile	Val	Lys	His	Val	Asp	
75																130	
77	gct	aag	aat	gtt	aca	att	att	gat	caa	tca	cct	cat	caa	ctt	gcc	aag	550
78	Ala	Lys	Asn	Val	Thr	Ile	Ile	Asp	Gln	Ser	Pro	His	Gln	Leu	Ala	Lys	
79																145	
81	gct	aga	aag	gaa	cct	ttg	aaa	gaa	tgt	aag	ata	ttg	gaa	gga	gat		598
82	Ala	Arg	Glu	Lys	Glu	Pro	Leu	Lys	Glu	Cys	Lys	Ile	Leu	Glu	Gly	Asp	
83																160	
85	gct	gag	gat	ttg	cct	ttt	cct	act	gat	act	ttt	gat	aga	tat	gtt	tct	646
86	Ala	Glu	Asp	Leu	Pro	Phe	Pro	Thr	Asp	Thr	Phe	Asp	Arg	Tyr	Val	Ser	
87																175	
89	gct	gga	agc	att	gag	tat	tgg	ccc	gat	cca	cag	cgc	ggt	atc	aag	gaa	694
90	Ala	Gly	Ser	Ile	Glu	Tyr	Trp	Pro	Asp	Pro	Gln	Arg	Gly	Ile	Lys	Glu	
91	180															195	
93	gca	tac	cga	gta	ctg	acc	ata	ggt	ggt	gtt	gcc	tgc	tta	ata	ggt	cct	742
94	Ala	Tyr	Arg	Val	Leu	Thr	Ile	Gly	Gly	Val	Ala	Cys	Leu	Ile	Gly	Pro	
95																210	
97	gtg	tac	ccg	acg	ttt	tgg	cta	tct	cgt	ttc	ttt	gca	gat	atg	tgg	atg	790
98	Val	Tyr	Pro	Thr	Phe	Trp	Leu	Ser	Arg	Phe	Phe	Ala	Asp	Met	Trp	Met	
99																225	
101	ctc	ttt	cca	aaa	gaa	gaa	gaa	tat	ata	gaa	tgg	ttc	aaa	aaa	gct	ggt	838
102	Leu	Phe	Pro	Lys	Glu	Glu	Glu	Tyr	Ile	Glu	Trp	Phe	Lys	Lys	Ala	Gly	
103																240	
105	ttc	gct	caa	gtt	aaa	ctc	aag	agg	att	ggc	cca	aaa	tgg	tat	cgt	ggt	886
106	Phe	Ala	Gln	Val	Lys	Leu	Lys	Arg	Ile	Gly	Pro	Lys	Trp	Tyr	Arg	Gly	
107																255	
109	gtc	cgt	cgc	cat	ggc	ttg	atc	atg	ggt	tgt	tct	gtg	act	ggt	gtc	aag	934
110	Val	Arg	Arg	His	Gly	Leu	Ile	Met	Gly	Cys	Ser	Val	Thr	Gly	Val	Lys	
111	260															275	
113	cca	tat	ttt	ggg	gaa	tct	ccg	ttg	cag	ctc	ggc	ccg	aag	gtt	gag	gat	982
114	Pro	Tyr	Phe	Gly	Glu	Ser	Pro	Leu	Gln	Leu	Gly	Pro	Lys	Val	Glu	Asp	
115																290	
117	gtg	agc	aag	cct	gta	aac	cca	ttc	gca	ttt	ctc	gtg	cga	ttc	ctc	ctc	1030
118	Val	Ser	Lys	Pro	Val	Asn	Pro	Phe	Ala	Phe	Leu	Val	Arg	Phe	Leu	Leu	
119																305	
121	ggc	ata	act	gct	gca	act	tat	tac	gtg	ctc	gtt	cca	ata	tac	atg	tgg	1078
122	Gly	Ile	Thr	Ala	Ala	Thr	Tyr	Tyr	Val	Leu	Val	Pro	Ile	Tyr	Met	Trp	
123																320	
125	ctc	aag	gat	caa	atc	acc	ccg	aaa	ggt	cag	cca	atc	tga	acaataagaa		1127	

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126 Leu Lys Asp Gln Ile Thr Pro Lys Gly Gln Pro Ile  
127 325 330 335  
129 gaacgtcaat ccaaagagaa gctctccaag cattctgttt gagagtacac cagtgaccac 1187  
131 aaatctatca cggaacaaga aagttttgg cgtcgttca agggtgaatt tgttgctta 1247  
133 gtttgttagt tttcagcct tagaaaggc cttttgtaaa gtttaatttc atggtaaaac 1307  
135 ctagaaatca ttgtgactat tttctagttg tataatctat cagtcatg 1355  
138 <210> SEQ ID NO: 2  
139 <211> LENGTH: 335  
140 <212> TYPE: PRT  
141 <213> ORGANISM: Nicotiana tabacum  
143 <400> SEQUENCE: 2  
145 Met Ala Ser Ser Ile Leu Ser Gly Ala Glu Asn Phe Lys Ile Leu Ser  
146 1 5 10 15  
149 Gly Ile Ser Pro Ser Glu Leu His Ile Lys Cys Phe Pro Gln Lys Gly  
150 20 25 30  
153 Leu Val Asn Tyr Ser Arg Ile Pro Asn Thr Lys Ser Arg Thr Leu Arg  
154 35 40 45  
157 Thr Lys Cys Ser Val Ser Ser Arg Pro Ala Ser Gln Pro Arg Phe  
158 50 55 60  
161 Ile Gln His Lys Lys Glu Ala Phe Trp Phe Tyr Arg Phe Leu Ser Ile  
162 65 70 75 80  
165 Val Tyr Asp His Val Ile Asn Pro Gly His Trp Thr Glu Asp Met Arg  
166 85 90 95  
169 Asp Glu Ala Leu Glu Pro Ala Glu Leu Asn Ser Arg Gln Leu Gln Val  
170 100 105 110  
173 Val Asp Val Gly Gly Thr Gly Phe Thr Thr Leu Gly Ile Val Lys  
174 115 120 125  
177 His Val Asp Ala Lys Asn Val Thr Ile Ile Asp Gln Ser Pro His Gln  
178 130 135 140  
181 Leu Ala Lys Ala Arg Glu Lys Glu Pro Leu Lys Glu Cys Lys Ile Leu  
182 145 150 155 160  
185 Glu Gly Asp Ala Glu Asp Leu Pro Phe Pro Thr Asp Thr Phe Asp Arg  
186 165 170 175  
189 Tyr Val Ser Ala Gly Ser Ile Glu Tyr Trp Pro Asp Pro Gln Arg Gly  
190 180 185 190  
193 Ile Lys Glu Ala Tyr Arg Val Leu Thr Ile Gly Gly Val Ala Cys Leu  
194 195 200 205  
197 Ile Gly Pro Val Tyr Pro Thr Phe Trp Leu Ser Arg Phe Phe Ala Asp  
198 210 215 220  
201 Met Trp Met Leu Phe Pro Lys Glu Glu Glu Tyr Ile Glu Trp Phe Lys  
202 225 230 235 240  
205 Lys Ala Gly Phe Ala Gln Val Lys Leu Lys Arg Ile Gly Pro Lys Trp  
206 245 250 255  
209 Tyr Arg Gly Val Arg Arg His Gly Leu Ile Met Gly Cys Ser Val Thr  
210 260 265 270  
213 Gly Val Lys Pro Tyr Phe Gly Glu Ser Pro Leu Gln Leu Gly Pro Lys  
214 275 280 285  
217 Val Glu Asp Val Ser Lys Pro Val Asn Pro Phe Ala Phe Leu Val Arg  
218 290 295 300

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221 Phe Leu Leu Gly Ile Thr Ala Ala Thr Tyr Tyr Val Leu Val Pro Ile  
 222 305 310 315 320  
 225 Tyr Met Trp Leu Lys Asp Gln Ile Thr Pro Lys Gly Gln Pro Ile  
 226 325 330 335  
 229 <210> SEQ ID NO: 3  
 230 <211> LENGTH: 1017  
 231 <212> TYPE: DNA  
 232 <213> ORGANISM: Arabidopsis thaliana  
 234 <220> FEATURE:  
 235 <221> NAME/KEY: CDS  
 236 <222> LOCATION: (1)..(1017)  
 238 <400> SEQUENCE: 3  
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 242 1 5 10 15  
 244 ggt tcc cct ggt tcc aat ttg cat gcc aaa tcg att cct ccg ccg acc 96  
 245 Gly Ser Pro Gly Ser Asn Leu His Ala Lys Ser Ile Pro Arg Pro Thr  
 246 20 25 30  
 248 tta ctc tca gtt acc cga acc tcc aca cct aga ctc tcg gtg gct act 144  
 249 Leu Leu Ser Val Thr Arg Thr Ser Thr Pro Arg Leu Ser Val Ala Thr  
 250 35 40 45  
 252 aaa tgc agc agc agc gtg tcg tct tcc ccg cca tcg gcg caa cct 192  
 253 Lys Cys Ser Ser Ser Val Ser Ser Ser Arg Pro Ser Ala Gln Pro  
 254 50 55 60  
 256 agg ttc att cag cac aag aag gag gct tac tgg ttc tac agg ttc tta 240  
 257 Arg Phe Ile Gln His Lys Lys Glu Ala Tyr Trp Phe Tyr Arg Phe Leu  
 258 65 70 75 80  
 260 tcc atc gta tac gac cat gtc atc aat cct ggg cat tgg acc gag gat 288  
 261 Ser Ile Val Tyr Asp His Val Ile Asn Pro Gly His Trp Thr Glu Asp  
 262 85 90 95  
 264 atg aga gac gac gct ctt gag cca gcg gat ctc agc cat ccg gac atg 336  
 265 Met Arg Asp Asp Ala Leu Glu Pro Ala Asp Leu Ser His Pro Asp Met  
 266 100 105 110  
 268 cga gtg gtc gat gtc ggc ggc gga act ggt ttc act act ctg ggc ata 384  
 269 Arg Val Val Asp Val Gly Gly Thr Gly Phe Thr Thr Leu Gly Ile  
 270 115 120 125  
 272 gtc aag aca gtg aag gcc aag aat gtg acc att ctg gac cag tcg cca 432  
 273 Val Lys Thr Val Lys Ala Lys Asn Val Thr Ile Leu Asp Gln Ser Pro  
 274 130 135 140  
 276 cat cag ctg gcc aaa gca aag caa aag gag ccg ttg aaa gaa tgc aag 480  
 277 His Gln Leu Ala Lys Ala Lys Gln Lys Glu Pro Leu Lys Glu Cys Lys  
 278 145 150 155 160  
 280 atc gtc gag gga gat gct gag gat ctt cct ttt cca acc gat tat gct 528  
 281 Ile Val Glu Gly Asp Ala Glu Asp Leu Pro Phe Pro Thr Asp Tyr Ala  
 282 165 170 175  
 284 gac aga tac gtt tct gct gga agc att gag tac tgg ccg gac ccg cag 576  
 285 Asp Arg Tyr Val Ser Ala Gly Ser Ile Glu Tyr Trp Pro Asp Pro Gln  
 286 180 185 190  
 288 agg gga ata agg gaa gca gcg tac agg gtt ctc aag atc ggt ggc aaa gcg 624

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289	Arg	Gly	Ile	Arg	Glu	Ala	Tyr	Arg	Val	Leu	Lys	Ile	Gly	Gly	Lys	Ala		
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292	tgt	ctc	atc	ggc	cct	gtc	tac	cca	acc	ttc	tgg	ctc	tct	cgc	ttc	ttt	672	
293	Cys	Leu	Ile	Gly	Pro	Val	Tyr	Pro	Thr	Phe	Trp	Leu	Ser	Arg	Phe	Phe		
294		210			215					220								
296	tct	gat	gtc	tgg	atg	ctc	ttc	ccc	aag	gag	gaa	gag	tac	att	gag	tgg	720	
297	Ser	Asp	Val	Trp	Met	Leu	Phe	Pro	Lys	Glu	Glu	Glu	Tyr	Ile	Glu	Trp		
298	225		230			235				240								
300	ttc	aag	aat	gcc	ggt	ttc	aag	gac	gtt	cag	ctc	aag	agg	att	ggc	ccc	768	
301	Phe	Lys	Asn	Ala	Gly	Phe	Lys	Asp	Val	Gln	Leu	Lys	Arg	Ile	Gly	Pro		
302		245			250					255								
304	aag	tgg	tac	cgt	ggt	gtt	cgc	agg	cac	gac	ctt	atc	atg	gga	tgt	tct	816	
305	Lys	Trp	Tyr	Arg	Gly	Val	Arg	Arg	His	Gly	Leu	Ile	Met	Gly	Cys	Ser		
306		260			265					270								
308	gtc	act	ggt	gtt	aaa	cct	gcc	tcc	ggt	gat	tct	cct	cag	ctt	ggt	864		
309	Val	Thr	Gly	Val	Lys	Pro	Ala	Ser	Gly	Asp	Ser	Pro	Leu	Gln	Leu	Gly		
310		275			280					285								
312	cca	aag	gaa	gag	gac	gta	gag	aag	cct	gtc	aac	aac	ccc	ttc	tcc	ttc	912	
313	Pro	Lys	Glu	Glu	Asp	Val	Glu	Lys	Pro	Val	Asn	Asn	Pro	Phe	Ser	Phe		
314		290			295					300								
316	ttg	gga	cgc	ttc	ctc	ctg	gga	act	cta	gca	gct	gcc	tgg	ttt	gtg	tta	960	
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318	305		310			315				320								
320	atc	cct	atc	tac	atg	tgg	atc	aag	gat	cag	atc	gtt	ccc	aaa	gac	caa	1008	
321	Ile	Pro	Ile	Tyr	Met	Trp	Ile	Lys	Asp	Gln	Ile	Val	Pro	Lys	Asp	Gln		
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329	<210>	SEQ	ID	NO:	4													
330	<211>	LENGTH:	338															
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334	<400>	SEQUENCE:	4															
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341		20				25				30								
344	Leu	Leu	Ser	Val	Thr	Arg	Thr	Ser	Thr	Pro	Arg	Leu	Ser	Val	Ala	Thr		
345		35				40				45								
348	Lys	Cys	Ser	Ser	Ser	Ser	Val	Ser	Ser	Ser	Arg	Pro	Ser	Ala	Gln	Pro		
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352	Arg	Phe	Ile	Gln	His	Lys	Lys	Glu	Ala	Tyr	Trp	Phe	Tyr	Arg	Phe	Leu		
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361		100				105					110							
364	Arg	Val	Val	Asp	Val	Gly	Gly	Thr	Gly	Phe	Thr	Thr	Leu	Gly	Ile			
365		115				120				125								

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L:17 M:270 C: Current Application Number differs, Replaced Current Application No

L:17 M:271 C: Current Filing Date differs, Replaced Current Filing Date